## AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

Claim 1 (currently amended): A method for identification of non-immunoglobulin peptides having an affinity for the surface of a fungus and an antifungal activity comprising:

(a) constructing a library of peptides by,
  (i) preparing random oligonucleotides;
  (ii) inserting said oligonucleotides into a vector that expresses peptides encoded by said random oligonucleotides on its surface and is capable of transfecting a host cell;
  (iii) transfecting a host cell with said vector to amplify said vector in an infectious form to create a library of peptides on the surface of said vector;
(b) contacting said vector expressing said peptide library with a target fungus and removing unbound vector;
(c) eluting bound vector from said fungus;
(d) amplifying said bound vector;
(e) sequencing the oligonucleotides contained in said eluted vector;
(f) deducing the amino acid sequence of peptides encoded by said oligonucleotides contained in said eluted vector; and
(g) selecting the non-immunoglobulin peptides having antifungal activity and for which the amino acid sequence has been deduced.

Claim 2 (previously presented): The method of any one of claims 1, 48, or 49 further comprising repeating steps (b) through (d) at least once.

Claim 3 (previously presented): The method of any one of claims 1, 48, or 49, wherein said vector is a fusion phage vector.

Claim 4 (previously presented): The method of any one of claims 1, 48, or 49, wherein said vector is a fusion phage vector selected from the group consisting of type 8, type 88, type 8+8, type 3, type 33, type 3+3, type 6, type 66, type 6+6, phage T7 and phage 8.

Claim 5 (previously presented): The method of any one of claims 1 or 48, wherein the sequence of said random oligonucleotide is GCA GNN (NNN)7 or SEQ ID NO: 1.

Claim 6 (previously presented): The method of any one of claims 1, 48, or 49, wherein said peptide is expressed as part of a coat protein of said vector.

Claim 7 (original): The method of claim 6, wherein said coat protein is a pIII or a pVIII coat protein.

Claim 8 (previously presented): The method of any one of claims 1, 48, or 49, further comprising determining the binding affinity of said peptides to said target fungus.

Claim 9 (previously presented): The method of any one of claims 1 or 48, wherein each of said peptides are of the same length, the length being 6 to 15 amino acids.

Claims 10 - 31 (canceled).

Claim 32 (previously presented): The method of any one of claims 1 or 49 wherein the target fungus is a plant pathogenic fungus.

Claim 33 (previously presented): The method of any one of claims 1 or 49 wherein the target fungus is a member of genus *Phytophthora*.

Claim 34 (previously presented): The method of any one of claims 1 or 49 wherein the target fungus is selected from the group consisting of *Phytophthora sojae*, *Phytophthora*

*capsici*, *Phytophthora cactorum*, *Phytophthora palmivora*, *Phytophthora cinnamomi*, *Phytophthora infestans,* and *Phytophthora parasitica*.

Claim 35 (previously presented): The method of any one of claims 1 or 49 wherein the target fungus is selected from the group consisting of *Phytophthora sojae*, *Phytophthora capsici*, *Phytophthora palmivora*, *Phytophthora cinnamomi*, and *Phytophthora parasitica*.

Claim 36 (previously presented): The method of any one of claims 1 or 49 wherein the target fungus is *Phytophthora sojae* or *Phytophthora capsici*.

Claim 37 (previously presented): The method of any one of claims 1, 48, or 49 wherein the vector expressing the peptide library is contacted with the target fungus at different life stages of the target fungus.

Claim 38 (previously presented): The method of any one of claims 1, 48, or 49 wherein the vector expressing the peptide library is contacted with the target fungus at oospore life stage or chlamydospore life stage.

Claim 39 (previously presented): The method of any one of claims 1, 48, or 49 wherein the vector expressing the peptide library is contacted with the target fungus at zoospore life stage.

Claim 40 (previously presented): The method of any one of claims 1, 48, or 49 wherein the vector expressing the peptide library is contacted with the target fungus at germling life stage.

Claim 41 (previously presented): The method of any one of claims 1 or 48 wherein each of said peptides are of a same length, the length being 8 amino acids.

Claim 42 (previously presented): The method of any one of claims 1 or 48 wherein the peptide library is an f8-1 peptide library.

Claim 43 (previously presented): The method of any one of claims 1 or 48 wherein each of said peptides are of a same length, the length being 15 amino acids.

Claim 44 (previously presented): The method of any one of claims 1 or 48 wherein the peptide library is an f88-4 peptide library.

Claim 45 (previously presented): The method of any one of claims 1, 48, or 49, further comprising repeating steps (b) through (d) at least twice.

Claim 46 (previously presented): The method of any one of claims 1, 48, or 49, further comprising repeating steps (b) through (d) at least three times.

Claim 47 (previously presented): The method of any one of claims 1, 48, or 49 wherein the bound vector is amplified in an *E. coli*.

Claim 48 (currently amended): A method for identification of non-immunoglobulin peptides having an affinity for the surface of a fungus and an antifungal activity comprising:

(a) constructing a library of peptides by,
    (i) preparing random oligonucleotides;
    (ii) inserting said oligonucleotides into a vector that expresses peptides encoded by said random oligonucleotides on its surface and is capable of transfecting a host cell;
    (iii) transfecting a host cell with said vector to amplify said vector in an infectious form to create a library of peptides on the surface of said vector;
(b) contacting said vector expressing said peptide library with a target fungus and removing unbound vector, wherein the target fungus is selected from

the group consisting of *Phytophthora sojae*, *Phytophthora capsici*, *Phytophthora palmivora*, *Phytophthora cinnamomi*, and *Phytophthora parasitica*;

(c) eluting bound vector from said fungus;

(d) amplifying said bound vector;

(e) sequencing the oligonucleotides contained in said eluted vector;

(f) deducing the amino acid sequence of peptides encoded by said oligonucleotides contained in said eluted vector; and

(g) selecting the non-immunoglobulin peptides having antifungal activity and for which the amino acid sequence has been deduced.

Claim 49 (currently amended): A method for identification of non-immunoglobulin peptides having an affinity for the surface of a fungus and an antifungal activity comprising:

(a) constructing a library of peptides by,

(i) preparing random oligonucleotides;

(ii) inserting said oligonucleotides into a vector that expresses peptides encoded by said random oligonucleotides on its surface and is capable of transfecting a host cell;

(iii) transfecting a host cell with said vector to amplify said vector in an infectious form to create a library of peptides on the surface of said vector;

wherein the library of peptides is (1) an f8-1 peptide library, wherein each peptide of the f8-1 peptide library has a length of 8 amino acids or (2) an f88-4 peptide library, wherein each peptide of the f88-4 peptide library has a length of 15 amino acids;

(b) contacting said vector expressing said peptide library with a target fungus and removing unbound vector;

(c) eluting bound vector from said fungus;

(d) amplifying said bound vector;

(e) sequencing the oligonucleotides contained in said eluted vector;

(f) deducing the amino acid sequence of peptides encoded by said oligonucleotides contained in said eluted vector; and

(g) selecting the non-immunoglobulin peptides having antifungal activity and for which the amino acid sequence has been deduced.

Claim 50 (previously presented): The method of claim 49 wherein the library of peptides is a f8-1 peptide library, wherein each peptide of the f8-1 peptide library has a length of 8 amino acids.

Claim 51 (previously presented): The method of claim 49 wherein the library of peptides is a f88-4 peptide library, wherein each peptide of the f88-4 peptide library has a length of 15 amino acids.